

1/34

				Motif 0	Motif 1	Motif 2	Motif 3 (A)
human				AKFLHMLMSVYVVELLRSFFYVTETTFQKNR			
tez1				ISETIEWVLGKRSNAKMCLSDFEKRKQIFAEEFTIYWLNSFILIPILQSFFYITESSDLRNR			
EST2				LKDFRWLFISD - IWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVT-			
p123				TREIISMQVET - SAKHFYYFDHEN - IYVLWKLLRWFEDLVSLIRCFYYVTEQQKSYSK	*	*	*
				*	*	*	*
human				LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRSLRFIPKP--DGL			
tez1				TVYFRKDIWKLLCRPF1-TSMKMEAFERKINENNVRMDTQK-TTLPPAVTRLLPKK--NTF			
EST2				IVYFRHDTWNKLITPPIVEYFKTYLIVENNVCRNHNSYTLS--NFNHSKMR1IPKKSNNEF			
p123				TYYYRKNIWDVIMKMS1-ADLKKTETLAEVQEKEVEEMKKS-LGFAPGKLRLIPKK--TTF	*	*	*
				*	*	*	*
human				RPIVNMDYVGARTFRREKRAERLTSRVKALF-SVLYNERA			
tez1				RLITN-LRKRFLIKMGSNKKM1VSTNQTLRPAVASTLKHLINESSSGIPFNLEVYMKL1TF			
EST2				RIIAIPCRGADEEEFTIYKENHNKA1QPTOKILEYLRNKRPTSFTK1Y5PTQIADRIKEF			
p123				RPIMTENKKIVNSDRKTTKLTTNTKLINSHMLKTLKN-RMFKDPPGFIAVFNYDDVMKRY	*	*	*
				*	*	*	*
human				KKDLLKHRMFGR-KKYFVRLIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATHATS			
tez1				KORLLKKFNNVNLPELYFMKFDVKSCYDSIPRMCEMRILKD-ALKNENGFFVRSQYFFNTN			
EST2				EEFVCKMKQVGQPQLFFATMDIEKCYDSDVNREKILSTFLKT"KLLSSDWFWINTAQILKRN	*	*	*
p123				*	*	*	*

FIG. 1

2/34

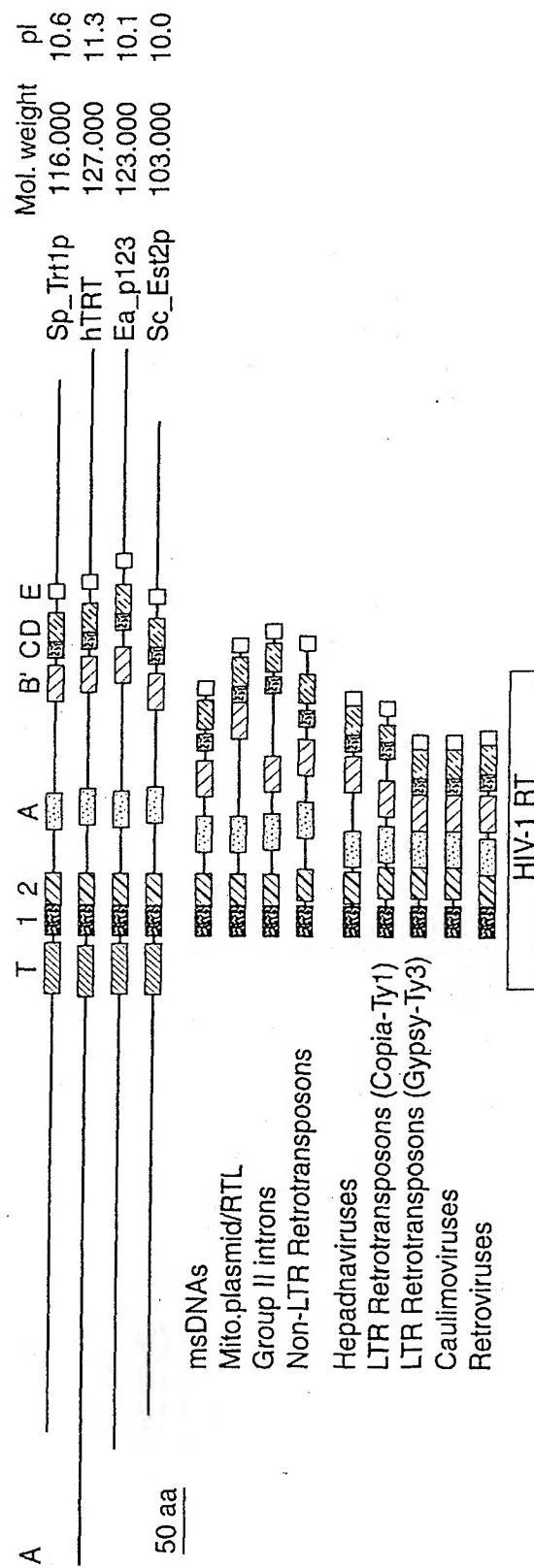


FIG. 2

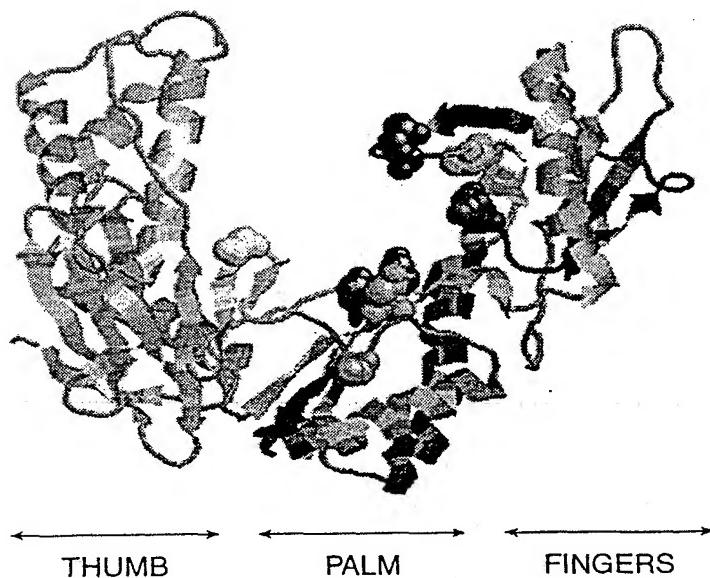


FIG. 3

2025 RELEASE UNDER E.O. 14176

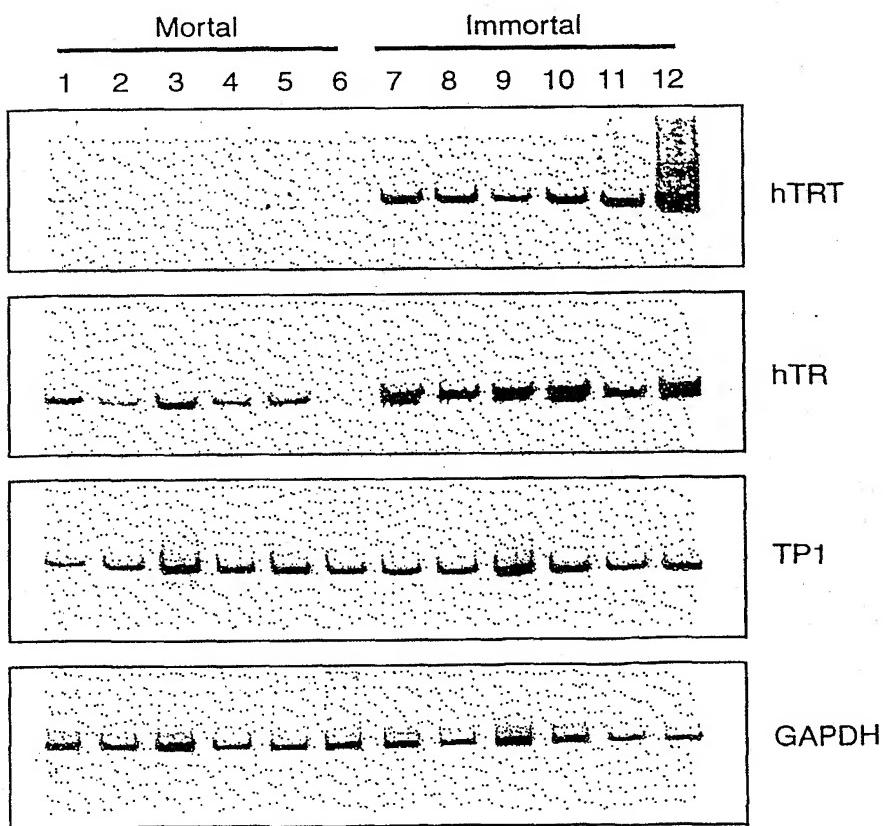


FIG. 5

**Motif T**

TRT con	WL	hh	hh	pFFY	TE	p	p	Y	RK	W	L	h	I	K
Sp_Tr1p	429	WL	YN	SFI	LI	PILQ	SFFY	IT	ESSD	DLR	NRTV	F	RK	I
hTrT	546	WL	MSV	VV	EL	LR	SF	YV	TET	FQ	KNR	L	FY	K
Ea_p123	441	WL	FE	DVV	SL	IR	CFF	YV	TE	QQ	SYS	KT	YY	RK
Sc_Est2p	366	WL	FRQ	LIP	KI	QT	FF	YC	TE	IS	STV	-IV	FRH	T

**Motif T'**

TRT con	K	Y	Q	GIPQGS	LS	hL	h	Y	DL	F				
Sp_Tr1p	6	YLQ	KVG	IP	QGS	SIL	SFL	CHY	ME	DLY	LSFT			
hTrT	5	SYV	QCQ	GP	QGS	SIL	STL	CS	YC	GDM	ENKL	FAGI		
Ea_p123	14	KFY	Q	TKG	IP	QGL	CVS	STL	SF	YAT	LE	SSLGFL		
Sc_Est2p	8	KCY	IRE	DGL	E	QGS	SSL	SAP	IVD	YDD	LFY	SEFK		

**Motif 1**

TRT con	h	h	hR	hR	PK	P	FR	I	h	K				
Sp_Tr1p	0	NN	VR	MT	QK	T	LL	PP	RL	KR	FL	IK	KK	LKD
hTrT	0	EV	RO	H	RE	AR	PL	LP	PL	RR	ER	LT	SL	82
Ea_p123	0	KE	VE	EW	KK	SL	GF	AP	GL	KL	PL	RT	FL	87
Sc_Est2p	1	CR	NH	NS	Y	TS	LN	HN	HS	KM	RI	PI	PK	68

**Motif 2**

RT con	P	hh	h	K	hR	h	hR	h	hR	h	R			
Sc_a1	0	LS	NEL	GTG	KFK	KPM	RVN	IP	KPK	GG	0	IRP	LSVG	NPDR
Dm_TART	0	SIL	RIG	YYP	DAW	KHA	QV	KM	LK	PGKS	6	YR	PSL	SGL
HIV-1	1	EG	KISK	I	GPN	PNT	PV	FA	IK	KKD	ST	WR	KLVD	RELNKRT

**Motif 3**

RT con	h	Y	DD	h	Y	DD	h	Y	DD	h	Y	DD	h	Y
Sc_a1	2	TYH	KPM	IGL	PQGS	SLI	SPIL	CNIV	ML	EDYI	55	VYR	YADD	LLIGVLGSKN
Dm_TART	6	RAG	QAG	GP	QGSN	LG	PILY	SIF	SSD	MPLPHIYHP	7	LSTYAD	DTIVL	SSDIL
HIV-1	4	GIR	QYN	VNL	PQG	WK	GSP	AI	QSSM	TKILEP	4	TYQYM	DDLY	VGSDLEIG

**Motif A**

TRT con	hnhK	hhdh	h	CDYD	I									
Sp_Tr1p	40	FGRK	KYF	VR	DI	K	SCYD	RI	KDLM	FR	IV	KK	LKD	82
hTrT	45	PPPE	LYFV	VKV	DVT	GAY	DTIP	QDRL	TE	VASII	IKP			87
Ea_p123	41	GQP	PKL	FF	ATM	DE	KCYD	SVN	REKL	STFL	KT	KL	100	
Sc_Est2p	42	VLP	ELXFM	KF	DVK	SCYD	SIP	PRM	CML	DKA	LN			68

**Motif B'**

TRT con	A	F	h	G	c	N	CK							
Sp_Tr1p	0	AK	KF	FL	LN	LS	RG	FEK	HNF	ST	SL	ELK	VI	181
hTrT	0	A	KTF	LR	TL	LL	V	RG	VEY	GC	VN	UR	KTV	197
Ea_p123	0	A	VL	TF	KL	LL	TT	Q	YCN	NG	FK	NM	KL	179
Sc_Est2p	0	F	IL	KL	IN	VS	RE	NG	FK	QY	NA	KA	NR	146

**Motif C**

TRT con	LLRL	DDFL	HT	A	F	h	G	c	N	CK					
Sp_Tr1p	6	LLR	VV	DD	FL	FT	VN	KK	0	AK	KF	FL	LN	17	
hTrT	5	LLR	LV	DD	FL	LV	TP	PHL	0	A	KTF	LR	TL	19	
Ea_p123	14	LMR	LT	DD	LL	LL	TT	Q	EN	0	A	VL	TF	KL	23
Sc_Est2p	8	IL	KL	AD	FL	LI	ST	DQ	Q	0	V	NI	KK	LA	20

**Motif D**

RT con	Gh	h	ck	h											
Sc_a1	2	KM	IK	RD	JNN	FL	NS	-I	GT	TM	NEE	KT	VI	4	
Dm_TART	6	NEN	YLK	T	FS	DW	AD	KW	G	IS	VN	AA	KTGH	25	
HIV-1	1	HRT	KIE	ELR	QH	LL	RW	GL	T	TPD	KHQ	0	EPP	FLMMG	1

**Motif E**

RT con	hLG	h												
Sc_a1	2	ESK	QSYL	GV	IL									
Dm_TART	6	EPP	FLMM	G	ITL									
HIV-1	1													

FIG. 4

5/34

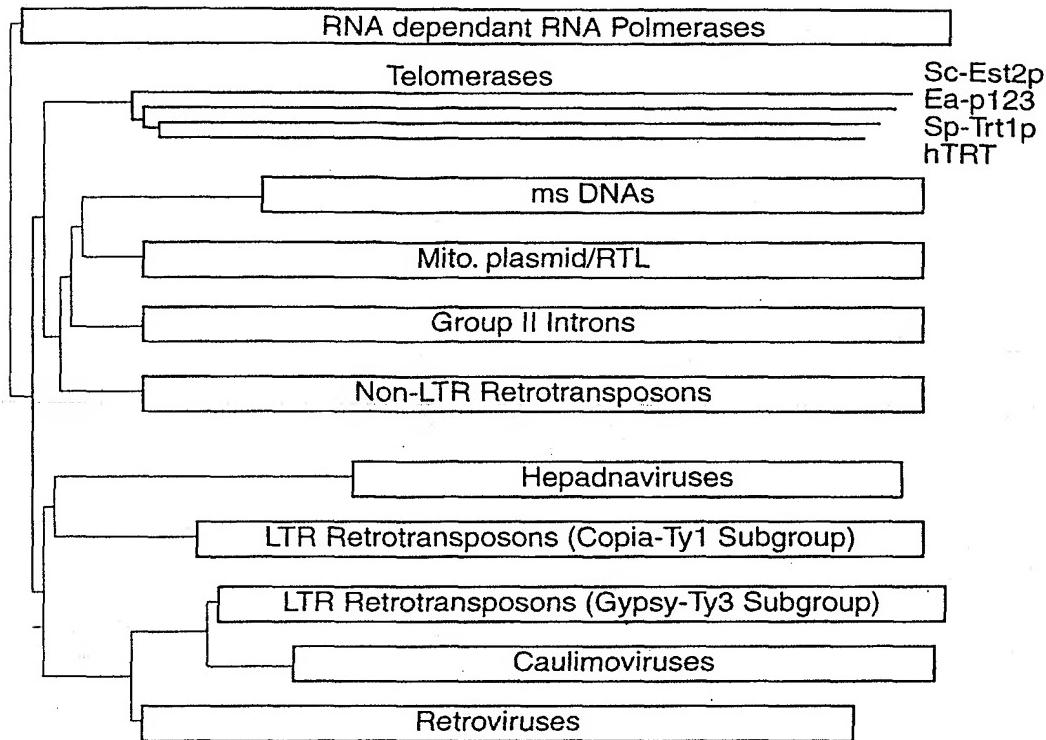


FIG. 6

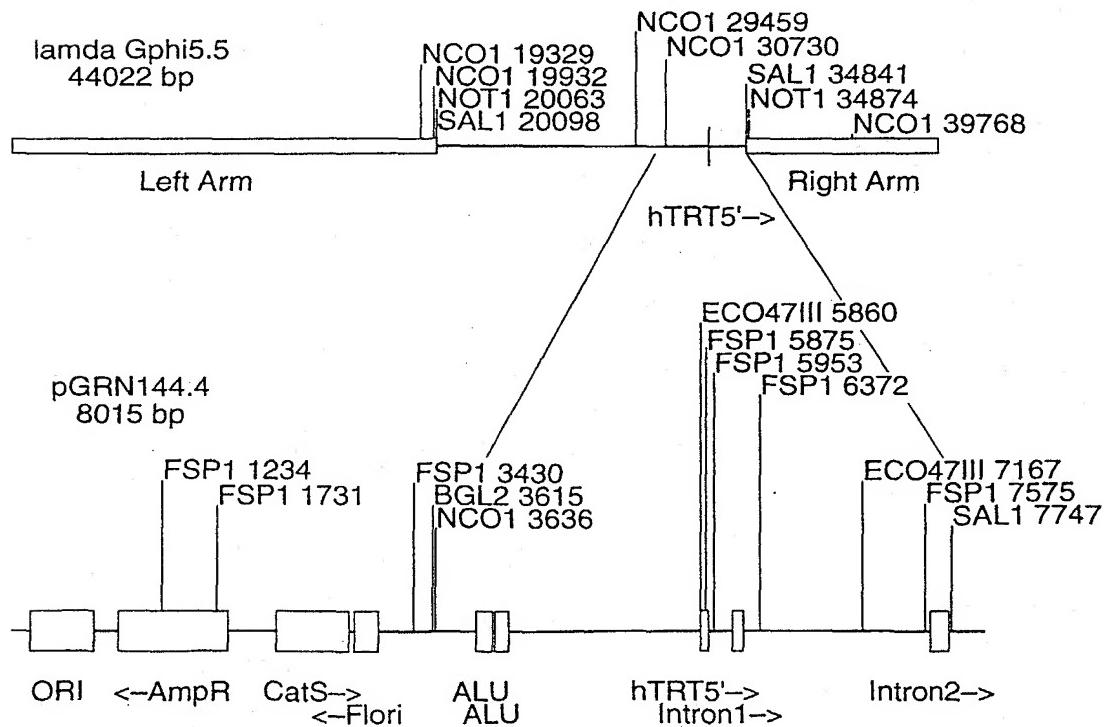


FIG. 7

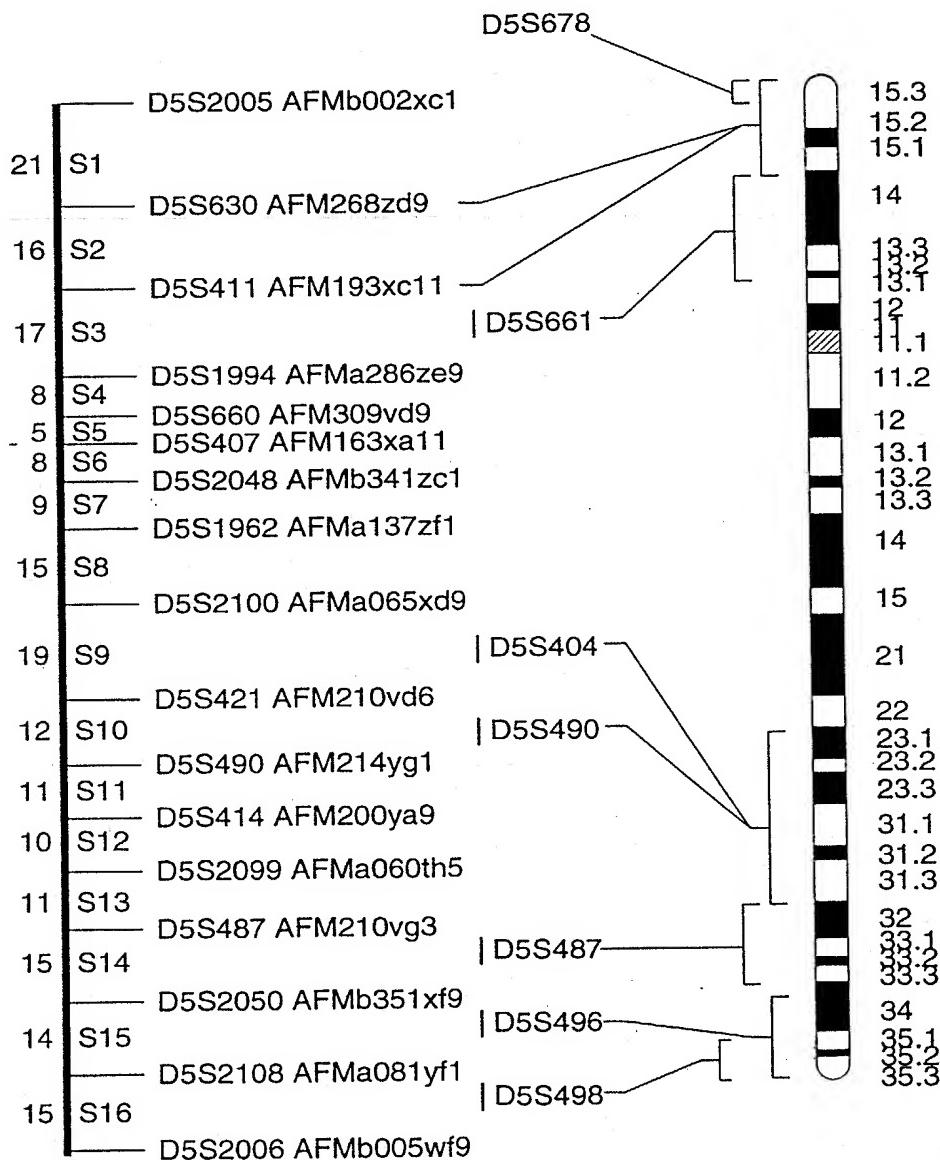


FIG. 8

7/34

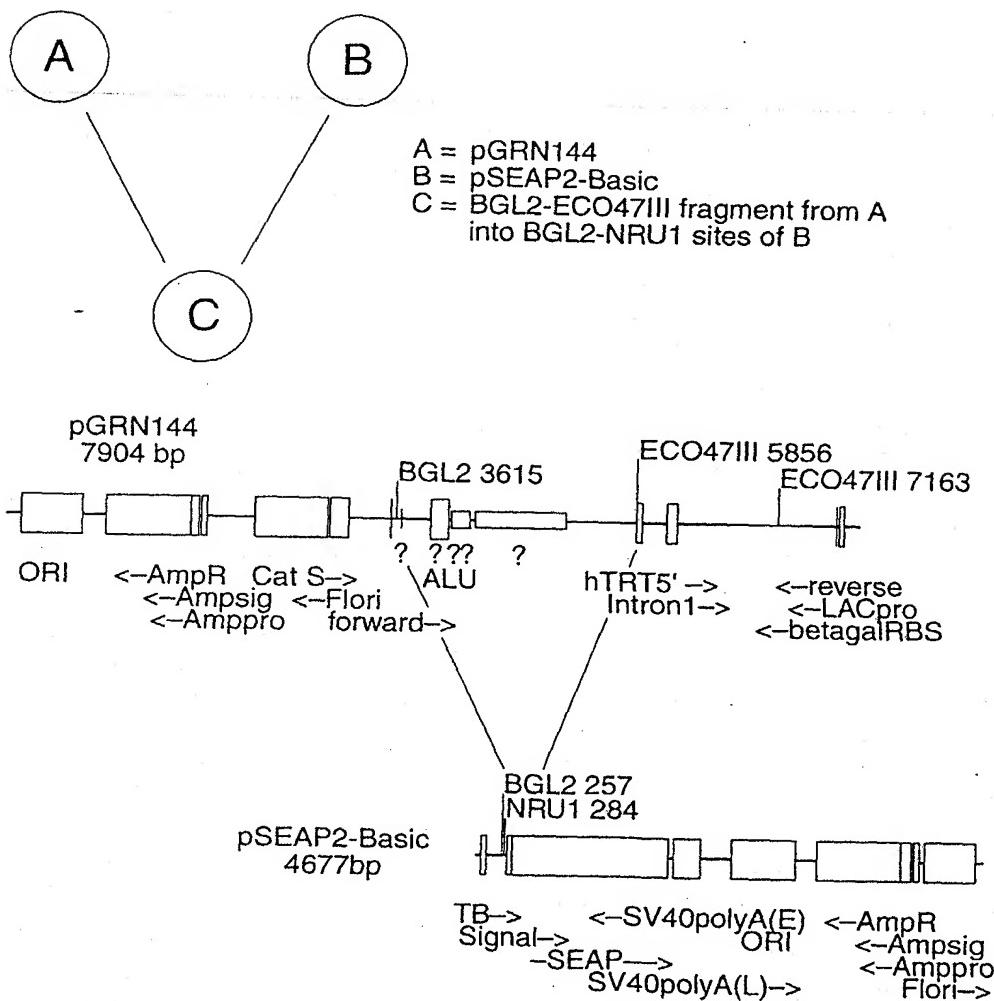


FIG. 9

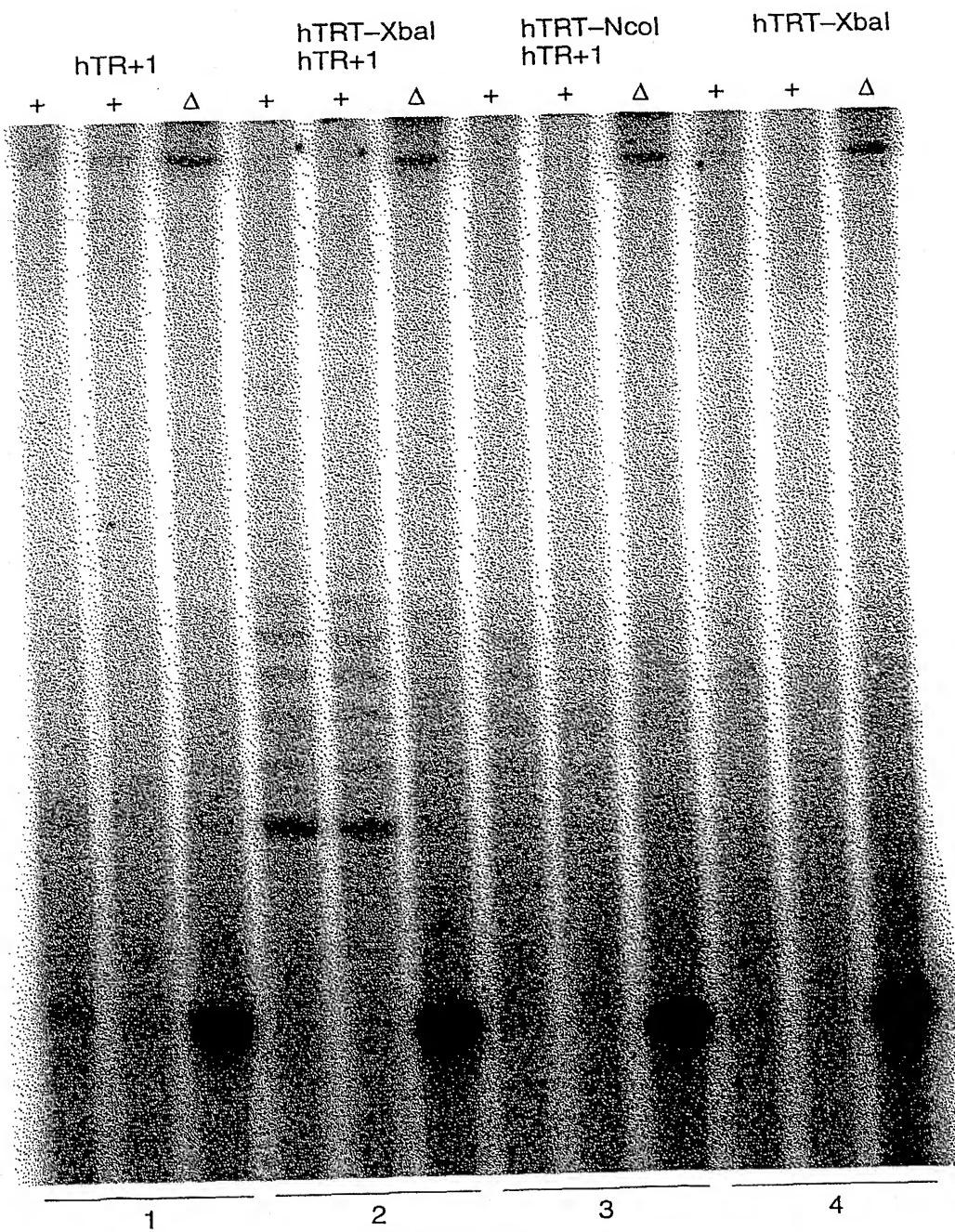


FIG. 10A

9/34

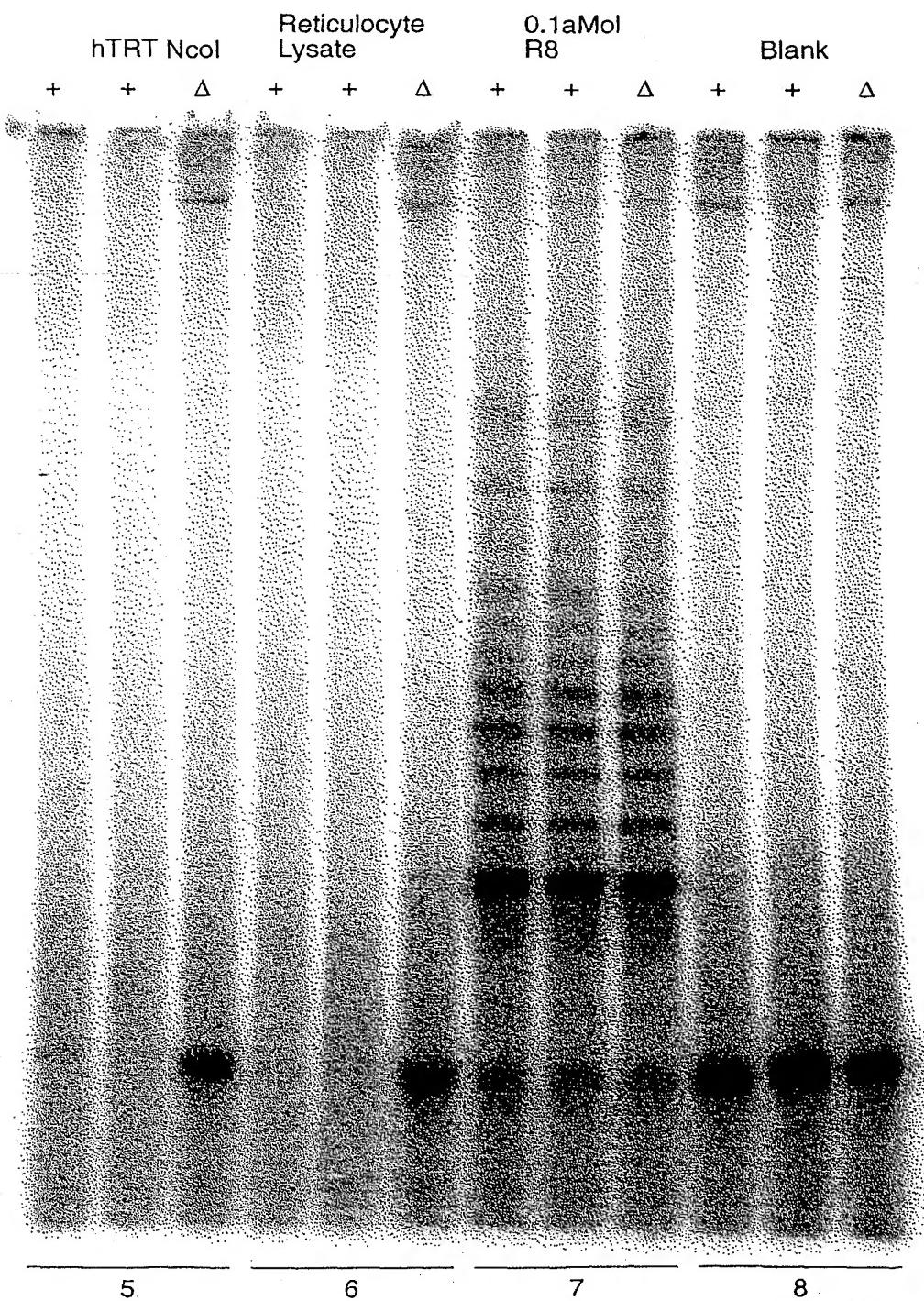


FIG. 10B

### Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	W1 FFY TE	Y Rk W 1 I E V
hTRT	546 WLMSVYVVELLRSFFFYVTETTFQKNRLLFFYRKSVWSKQLQSIGI	13 EAEVRI
SPTRT	429 WLYNSFLIPILQSQFFVTEESSDRLRNRTVYFRKDIWKLLCRPF	12 ENIVR
Ea_p123	441 WLFEDLWVSLIRCFYYVTEQQKSYSKTYYYRKNIWDVIMKMSI	12 EKEVE
Sc_Est2	366 WLFRQLIPKLIQQTFFYCTEISSTVT.IVYFRHDTWNKLITPFI	9 ENIVC

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKK	FR I	P LYF D CYD i	Y q GipQGS 1S 1 Y
hTRT	11 SRLRFIPKPDG	0 LRPIV	69 PELYFKVVDVTGAYDTI	104 YVQCQGIPQGSILSTLLCSLCY
SPTRT	10 AVIRLIPKNT	0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPQGSILSSFLCHFYM
Ea_p123	10 GKRLIPKKTT	0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSSILSSFYV
Sc_Est2	13 SKMRLIPKKSN	2 FRIIA	68 PELYFMKFDVVKSCYDSI	85 YIREDGFLFQGSSLSSAPIVDLVY
RT con	p hh h K	hR h	h hDh AF h	hPQG pp nh h GY

### Telomerase RT Motifs (Fingers)

	MOTIF C	MOTIF D	MOTIF E
TRT con	111rl1 DDFL it	g n K	w g s 1
hTRT	15 LLRLRVDDFLLT	15 GVPEYGCVVLRLKTVV	24 WCGLLLDTRTL 192
SPTRT	16 VLRLRVDDFLFIT	15 GFEKHNFSTSLEKTVI	22 FFGFSVNMRSL 176
Ea_p123	24 LLMLRLDDYLLIT	15 VSRENGFKFNMKKKLOT	28 WIGISIDMKTL 174
Sc_Est2	18 LIKLADDFLIIS	15 GFQKYNAKANRDKILA	25 WKHSSTMNNFH 141
RT con	h Y DDhhh	Gh h CK h	hLG h F

F/G. 11

181 GGACCCGGCGGCTTCCGCGCCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGACGC  
CCTGGGCCCGAAAGGCGCGACCACGGGTACGGACCACACGCACGGACCCCTGCG

NFKB\_CS1  
GGGRQTYYQC  
NFkB-MHC-I.2  
TGGGCTTCCCC  
\*\*\*\*\*

241 ACGGCCGCCCCCGCCGCCCTCCTCCGCCAGGTGGGCCTCCCCGGGTCGCGTCCG  
TGCCGGCGGGGGCGGGAGGAAGGCGGTCCACCCGGAGGGGCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGCCGGGGGAACCAGCGACATCGGGAGAGCAGCGCAGGCACTC  
CGACCCCAACTCCCGCCGGCCCCCTGGTCGCTGTACGCCCTCGTCGCGTCCGCTGAG

NFKB\_CS1  
GGGRQTYYQC  
NFkB\_CS2  
RGGGRMTYYCC  
Topo\_II\_cleavage\_site  
RNYNNCNNGYNGKTNINY  
\*\*\*\*\*>

361 AGGGCGCTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG  
TCCC CGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACGGCTACGACGTCTCC

FIG. 12

1 AAAACCCCAA AACCCCAAAA CCCCTTTAG AGCCCTGCAG TTGGAAATAT  
51 AACCTCAGTA TTAATAAGCT CAGATTTAA ATATTAATTA CAAAACCTAA  
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC  
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGA  
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAAGAT  
251 TTAGAAGATA TTAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG  
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT  
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTCA  
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTCAA  
501 CTCAAAAGCA GTATTTCTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATCCA  
601 GCGAACTTCT GAAGGAACCTC TTGTTCAATT TTGCGGGAA AACGTTTTG  
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA  
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
751 GAATGAGAAA GATCACTTTC TCAACAAACAT CAACGTGCCG AATTGGAATA  
801 ATATGAAATC AAGAACCGAGA ATATTTTATT GCACCTCATTT TAATAGAAAT  
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTC  
901 AGCGATGGAC AGAGCTCAGA CGATATTAC GAATATATTG AGATTTAATA  
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG  
1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTT  
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA AAAAAAAATC GAAAACCTGA  
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC  
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA  
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTT  
1251 AAAAGAAAGT TAAGAAATAT GTGGAACCTAA ACAAGCATGA ACTCATTCAC  
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT  
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGGATCT CGTCGTCTCG  
1451 CTGATTAGAT GATTTTTCTA TGTCAACCGAG CAACAGAAAA GTTACTCCAA  
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
1551 TCGCAGACTT AAAGAAGGAA ACCGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGAAAAC TCAGACTAAT  
1651 ACCGAAGAAA ACTACTTCC GTCCAATTAT GACTTCAAT AAGAAGATTG  
1701 TAAATTCAGA CGGAAAGACT AAAAAATTAA CTACAAATAC GAAGTTATTG  
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC  
1801 TTTTGATTTC GCTGTTTTA ACTATGATGA TGTAATGAA AAGTATGAGG  
1851 AGTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTGCA  
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC  
1951 AACATTCCA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA  
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAC  
2051 TTTAGAAAGA AAGAAATGAA AGATTATTT AGACAGAAAT TCCAGAAGAT  
2101 TGCACATTGAA GGAGGACAAT ATCCAACCTT ATTCACTGTGTT CTTGAAAATG  
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA  
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCACTCA TTAATATTTG  
2251 CCAATATAAT TACATTAAC TTAATGGGA GTTTTATAAA CAAACAAAAG  
2301 GAATTCCCTCA AGGTCTTGA GTTTCATCAA TTTTGTCTC ATTTTATTAT  
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTG CTTAGAGATG AATCAATGAA

FIG. 13

2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTTGACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTAATGAA TAACATTACC  
2801 CATTATTTA GAAAGACGAT TACAACCGAA GACTTGCAG ATAAAACCTCT  
2851 CAACAAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAAGGA CCACTTTAACG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAAAATAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATTTC TGGAGAGGAG CATTATCCAG  
3051 ACTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTGGA AAGTTAATT TCAATTTCG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

*FIG. 13*  
(CONTINUED)

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD  
51 LEDIKIFQAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFORTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM  
301 LEVKDFNFN YYLTOKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH  
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKL RWIFEDLVVS  
451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV  
501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL  
551 NSHMLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN  
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ  
701 RNYFKKDNLQ QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSIILSSFYY  
751 ATLEESSSLGF LRDESMNPEN PNVLLLMRLT DDYLLITTQE NNAVLFIEKL  
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTALM PNINLRIEGI LCTLNLMQTT KKASMWLKKK LKSFLMNNIT  
901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID  
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK  
1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

*FIG. 14*

FIG. 15

1470	GAT	CTC	GTT	TCT	ACT	TTT	CCT	AAT	TAC	CCT	ATA	TCT	TAA	AAA	AAT	TGG	CAA	1529			
129	D	L	V	S	T	F	P	N	Y	L	I	S	I	L	E	S	K	N	W	Q	148
1530	CTT	TTG	TTA	GAA	AT	gtaaaataccggtaaaggatgtgcgactttgaacpagactgtatacgacaatggtag	T	ATC	GGC	1601	I	G	155								
149	L	L	L	E	I																
1602	AGT	GAT	GCC	ATG	CAT	TAC	TTA	TAA	TCC	AAA	GGA	AGT	ATT	TTT	GAG	GCT	CCT	CCA	AAT	GAC	1661
156	S	D	A	M	H	Y	L	L	S	K	G	S	I	F	E	A	L	P	N	D	175
1662	AAT	TAC	CTT	CAG	ATT	TCT	GCC	ATA	CCA	CTT	TTT	AAA	AAT	ATT	GTG	TTT	GAG	GAA	ACT	GTG	1721
176	N	Y	L	Q	I	S	G	I	P	L	F	K	N	N	V	F	E	E	T	V	195
1722	TCA	AAA	AAA	AGA	AAG	CGA	ACC	ATT	GAA	ACA	TCC	ATT	ACT	CAA	AAT	AAA	AGC	GCC	CGC	AAA	1781
196	S	K	K	R	R	T	I	E	T	S	I	T	Q	N	K	S	A	R	K	215	
1782	GAA	GTT	TCC	TGG	AAT	AGC	ATT	TCA	ATT	AGT	AGG	TTT	AGC	ATT	TTT	TAC	AGG	TCA	TCC	TAT	1841
216	E	V	S	W	N	S	I	S	I	S	R	F	S	I	F	Y	R	S	S	Y	235
1842	AAG	AAG	TTT	AAG	CAA	G	gtaaactaatactgttatccataactaaacttttag	AT	CTA	TAT	TTT	AAC	1907								
236	K	K	F	K	Q	D								L	Y	F	N				245
1908	TTA	CAC	TCT	ATT	TGT	GAT	CGG	AAC	ACA	GTA	CAC	ATG	TGG	CTT	CAA	TGG	ATT	TTT	CCA	AGG	1967
246	L	H	S	I	C	D	R	N	T	V	H	M	W	L	Q	W	I	F	P	R	265
1968	CAA	TTT	GGA	CTT	ATA	AAC	GCA	TTT	CAA	GTG	AAG	CAA	TTG	CAC	AAA	GTG	ATT	CCA	CTG	GTA	2027
266	Q	F	G	L	I	N	A	F	Q	V	K	Q	L	H	K	V	I	P	L	V	285
2028	TCA	CAG	AGT	ACA	GTT	GTG	CCC	AAA	CGT	CTC	CTA	AAG	GTA	TAC	CCT	TTA	ATT	GAA	CAA	ACA	2087
286	S	Q	S	T	V	V	P	K	R	L	L	K	V	Y	P	L	I	E	Q	T	305
2088	GCA	AAG	CGA	CTC	CAT	CGT	ATT	TCT	CTA	TCA	AAA	GTT	TAC	AAC	CAT	TAT	TGC	CCA	TAT	ATT	2147
306	A	K	R	L	H	R	I	S	L	S	K	V	Y	N	H	Y	C	P	Y	I	325
2148	GAC	ACC	CAC	GAT	GAA	AAA	ATC	CTT	AGT	TAT	TCC	TTA	AAG	CCG	AAC	CAG	GTG	TTT	GCG	2207	
326	D	T	H	D	D	E	K	I	L	S	Y	S	L	K	P	N	Q	V	F	A	345
2208	TTT	CTT	CGA	TCC	ATT	CTT	GTT	CGA	GTG	TTT	CCT	AAA	TTA	ATC	TGG	GGT	AAC	CAA	AGG	ATA	2267
346	F	L	R	S	I	L	V	R	V	F	P	K	L	I	W	G	N	Q	R	I	365

FIG. 15  
(CONTINUED)

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaatttaccactaaacgattttaccag AC CTC GAA ACT 2336  
366 F E I I L K D L E T 375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396  
376 F L K S R Y E S F S L H Y L M S N I K 395

2397 gtaatatgcaccaatttttaccataataacaatcg ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465  
396 I S E I E W L V L G 405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA ACT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525  
406 K R S N A K M C L S D F E K R K Q I F A 425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TAT 2585  
426 E F I Y W L Y N S F I I P I L Q S F F Y 445

2586 ATC ACT GAA TCA ACT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645  
446 I T E S S D L R N R T V Y F R K D I W K 465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705  
466 L C R P F I T S M K M E A F E K I N E 485

2706 gtattttaaagtttttggaaaaaggcttaataattttcac AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775  
486 N N V R M D T Q K T 495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAT ACC TTT CGT CTC ATT ACG 2835  
496 T L P P A V I R L L P K K N T F R L I T 515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaaattttggtcataatgtactttacttataatcttata 2906  
516 N L R K R F L I K 524

2907 ttagcag ATG GGT TCA AAC AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967  
525 M G S N K K M L V S T N Q T L R P V 542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027  
543 A S I L K H L I N E E S S G I P F N L E 562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088  
563 V M K L L T F K D L K H R M F G 581

FIG. 15  
(CONTINUED)

17/34

3089 tataataatgcgcgatccctcatttgcag G CGT AAG TAT TTT GTA CGG ATA GAT ATA  
582 R K K Y F V R I D I 3155  
3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC  
592 K S C Y D R I K Q D L M F R I V K K L 3215  
3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT  
612 K D P E F V I R K Y A T I H A T S D R A 631  
3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttattttcattggaaatttttaacaa 3343  
632 T K N F V S E A F S Y F 643  
3344 atttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA  
644 D M V P F E K V V Q L L S M K T 3405  
3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT  
660 S D T L F V D F V D Y W T K S S E I F 3465  
3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattttaaca 3532  
680 K M L K E H L S G H I V K 692  
3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CCT CTT CAA AAA GTC GGT ATC CCT CAG GGC TCA  
693 T G N S Q Y L Q K V G I P Q G S 3593  
3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG  
709 I L S S F L C H F Y M E D L I D E Y L S 3653  
3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA  
729 F T K K G S V L L R V D D F L F I T 748  
3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gttagtgtgtgtcattcc 3777  
749 V N K K D A K K F L N L S L R G 764  
3778 taagtcttaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA  
765 F E K H N F S T S L E K T V 3840  
3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA  
779 I N F E N S N G I I N N T F F N E S K K 3900  
798

F/G. 15  
(CONTINUED)

18/34

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960  
799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA AAC TCA TTT AAC TCT ACA TCT GTC GAG CTG ACG AAA CAT ATG GGG 4020  
819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TAC AAA ATT CTA AG gtatactgttaactgacaaataatcg A TCG 4089  
839 K S F F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149  
849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209  
869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gttagtacttttaactaga 4274  
889 R M K D I F I P Q R M F I T D 903

4275 aaagtccattaaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339  
904 L L N V I G R K I W K K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401  
918 E I L G Y T S R R F L S S A E V K W 935

4402 ggctctcgagacttcaggcaatattgacacatcg G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468  
936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528  
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA CAT AGA AGA ATA 4588  
967 D L I K P L R P V L R Q V L F L H R R I 986

4589 GCT GAT TAA tgcattttcaattatacatccctttattactgggttcaatattactaaatataatcgat 4665  
987 A D \* 989

FIG. 15  
(CONTINUED)

19/34

FIG. 15  
(CONTINUED)

20/34

FIG. 16

MPRAPRCAVRSLRLSHYREVPLATFVRLGPQGWRLVQRGDP  
AAFRALVAQCLVCVPWDARPPPAAPSFRQSVCLKEVARVLQRL  
CERGAKNVLAFGFALLDARGGGPEAFTTSVRSYLPNTVDALAR  
GSGAWGLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY  
QLGAATQARPPPHASGPERRLGCEAWNHSVREAGVPLGLPAPG  
ARRRGGSASRSLPLPKRPRRGAAPEPERTPVQGSWAHPGRTRG  
PSDRGFCVSPARPAEATSLEGALSGTRSHPSVGRQHHAGPP  
STSRRPPWDTPCPVVAETKHFYVSSGDEQLRPSFLLSSLRP  
SLTGARRLVEIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL  
LGNHAQCPYGVLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEE  
EDTDPRRLVQLLRQHSSPWQVYGFVRACLRLVPPGLWGSRHNE  
RRFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGC  
VPAAEHRLREEILAKFLHWLMSVYVVELRSFFYVTETTFQKNR  
LFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAL  
LTSRLRFIPKPDGLRPIVNMDYVVGARTFREKRAERLTSRVKA  
LFSVLNYERARRPGGLGASVGLDDIHRRAWRTFVLRVRAQDPPP  
ELYFVKVDVTGAYDTIPQDRLTEVIASIICKPONTYCVRYYAVVQ  
KAAAHGHRKAKFHKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVI  
EQSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSI  
LSTLLCSLCYGD MENKLFAGIRDG LLLRLVDDFLVTPHLTHA  
KTFLRTLVRGVPEYGC VVNL RKTVVNF PVEDE ALGGT AFVQMPA  
HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLT FNRGFKAGR  
NMRRKLFGVRLRKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRF  
HACVLQLPFHQQVWKNPFFLRVISDTASLCYSILKAKNAGMSL  
GAKGAAGPLPSEAVQWLCHQAFLLKLT RHRVTVPLLGSRLTAQ  
TQLSRKLPGTTLTALEAAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTCAGTCGAGCTGCTCAGGTCTTTCTT  
TTATGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTCTACCGGAAGAGTGTCTG  
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAAGAGGGTGCAGCTGCCAGCT  
GTCGGAAGCAGAGGTCAAGCAGCATCGGGAGCCAGGCCGCTGACGTCCAGACT  
CCGCTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGG  
AGCCAGAACGTTCCGAGAGAAAAGAGGGCGAGCGTCTCACCTCGAGGGTGAAGGCACT  
GTCAGCGTCTCAACTACGAGCGGGCGCGCCCGCTCTGGCGCCTCTGTGCT  
GGGCTGGACGATATC ACAGGGCTGGCGCACCTTCTGTGCGTGTGCGGGCCAGGA  
CCCGCCGCTGAGCTGACTTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATCCC  
CCAGGACAGCCTCACGGAGGTACCGCACATCATCAAACCCCCAGAACACGTA CTGCGT  
GCCGCGTATGCCGTGTCAGAGGGCCCATGGCACGTCGGCAAGGCCCTCAAGAG  
CCACGCTCTACGTCAGTGCAGGGGATCCCGAGGGCTCCATCTCTCACGCTGCTCT  
GCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCGGGGATT CGCGGGACGGC  
TGCTCCTGCGTTGGGGATGATTCTTGTGGT GACACCTCACCTCACCCACCGCGAAA  
CCTCCTCAGGACCTGGTCCAGGTGTCCCTGAGTATGGCTGGTGAAC TTGCGGA  
AGACAGTGGTGAACTTCCCTGTTAGAACAGCAGGCCCTGGTGGCACGGCTTTGTTCAA  
TGCCGGCCACGGCCTATTCCCTGGTGCAGGCCCTGCTGCTGGATACCCGGACCCCTGGAGG  
TGCAGAGCGACTACTCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCACCTTCAACC  
GGGGCTTCAAGGCTGGGAGGAACATCGCTGCAAACACTTTGGGGCTTGGCTGAAGT  
GTCACAGCCTGTTCTGGATTTGAGGTGACAGGTTCA CGCATGTGTGCTGCAGCTCCCATT  
ACAAGATCCTCCTGCTGAGGCGTACAGGTTCA CGCATGTGTGCTGCAGCTCCCATT  
ATCAGCAAGTTGGAGAACCCCCACATTTCCTGCGCGTCACTCTGACACGGCCTCCC  
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAAGGGATGTCGCTGGGGCCAAGGGCG  
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC  
TGACTCGACACCGTGCACCTACGTGCCACTCCTGGGTCACTCAGGACAGGCCAGACGC  
AGCTGAGTCGGAAGCTCCGGGACGCGTGA CTCAGTGCCTGGAGGCCAGCCAACCCGG  
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGCCACCCGCCACAGCCAGGCC  
AGAGCAGACACCAGCAGGCCCTGTCA CGCCGGCTCACGTCCCAGGGAGGGAGGGGG  
CCACACCCAGGCCCTGCACCGCTGGAGCTGAGGCTGAGTGAGTGTGAGGCTGAGCC  
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGG  
TGAGTGTCCAGCACACTGCCGTCTTCACTTCCCACAGGCTGGCGCTGGCTCCACCC  
AGGGCCAGCTTCTCACCAGGAGGCCGCTTCACTTCCCACATAGGAATAGTCCATC  
CCCAGATTGCCATTGTTCACCCCTGCCCTGCCCTCTTGCCTTCCACCCCCACCATC  
CAGGTGGAGACCCCTGAGAAGGACCTGGAGCTGAGTGGAAATTGAGTGACCAAAGGTGT  
GCCCTGTACACAGGCAGGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGG  
GGAGGTGCTGGAGTAAAATACTGAATATGAGTTTCAGTTTG0AAAAAAAAAAAA  
AAAAAAAAAAAAAA

FIG. 18

MetSerValTyrValValGluLeuLeuArgSerPhePhe  
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe  
PheTyrArgLysSerValTrpSerLysLeuGlnSerIle  
GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu  
LeuSerGluAlaGluValArgGlnHisArgGluAlaArg  
ProAlaLeuLeuThrSerArgLeuArgPheIleProLys  
ProAspGlyLeuArgProIleValAsnMetAspTyrVal  
ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu  
ArgLeuThrSerArgValLysAlaLeuPheSerValLeu  
AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla  
SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg  
ThrPheValLeuArgValArgAlaGlnAspProProPro  
GluLeuTyrPheValLysValAspValThrGlyAlaTyr  
AspThrIleProGlnAspArgLeuThrGluValIleAla  
SerIleIleLysProGlnAsnThrTyrCysValArgArg  
TyrAlaValValGlnLysAlaAlaHisGlyHisValArg  
LysAlaPheLysSerHisValLeuArgProValProGly  
AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln  
ProValLeuArgArgHisGlyGluGlnAlaValCysGly  
AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

1  
met

GCAGCGCTGCGTCCTGCTGCGCACGTGGAAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40

phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

50

ala arg pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60

leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TCG CTG GAC GGG

80

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90

100

110

120

FIG. 20

130

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140

trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160

leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CTC TAC CAG CTC GGC GCT GCC

180

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

190

leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

210

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

220

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

230

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

240

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

250

val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

260

gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

270

gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CGT CCC

280

trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

290

300

310

320

330

*FIG. 20*  
(CONTINUED)

340

leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350

leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

360

glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

370

arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro  
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

380

leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

390

val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

400

ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

410

ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

420

leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

430

ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

440

his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

450

leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

460

met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

470

gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG GAG GAG ATC CTG

480

490

500

510

520

530

540

FIG. 20  
(CONTINUED)

550

ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560

leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580

arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590

ile gly ile arg gln his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610

ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620

leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640

pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650

arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660

phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGC CCC GGC CTC CTG

680

gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700

thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG

710

tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730

gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC AAA CCC CAG

740

asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750

FIG. 20  
(CONTINUED)

760  
his gly his val arg lys ala phe lys ser his val leu arg pro  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770  
val pro gly asp pro ala gly leu his pro leu his ala ala leu  
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

780  
gln pro val leu arg arg his gly glu gln ala val cys gly asp  
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

790  
ser ala gly arg ala ala pro ala phe gly gly OP  
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGGTGGT

GACACCTCACCTCACCCACCGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA

GTATGGCTGCGTGGTGAACTTGCCGAAGACAGTGGTGAACCTCCCTGTAGAACAGCAGGC

CCTGGGTGGCACGGCTTTGTTCAGATGCCGGCCACGGCCTATTCCCTGGTGCGGCCT

GCTGCTGGATAACCGGACCCCTGGAGGTGCAGAGCAGACTCCAGCTATGCCGGACCTC

CATCAGAGCCAGTCTCACCTCAACCGCGCTCAAGGCTGGAGGAACATGCGTCGCAA

ACTCTTGGGTCTGCCGCTGAAGTGTACAGCCTGTTCTGGATTTGCAGGTGAACAG

CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGGTACAGGTTCA

CGCATGTGTGCTGCAGCTCCATTCTACAGCAAGTTGGAAGAACCCCACATTTCCCT

GCAGCGTCATCTCTGACACGGCCTCCCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG

GATGTCGCTGGGGCCAAGGGCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT

GTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCCT

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGAC

TGCCCTGGAGGCCGAGCCAACCCGGCACTGCCCTCAGACTCAAGACCACCTGGACTG

ATGGCCACCCGCCACAGCCAGGCCAGAGCAGACACCAGCAGGCCCTGTCACGCCGGCT

CTACGTCCCAGGGAGGGAGGGCGCCGGCCACACCCAGGCCGACCGCTGGAGTCTGAGG

CCTGAGTGAGTGTGTTGCCGAGGCCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG

GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCAGCACACCTGCCGTCTTCACTTCCC

CACAGGCTGGCGCTGGCTCCACCCAGGGCCAGCTTCTCACCAGGAGGCCGGCTTC

CACTCCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTTCACCCCTGCCCTGCC

CTCCTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCCTGAGAAGGACCCCTGGAGCTC

TGGGAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGCCCTGCACCTGGAT

GGGGTCCCTGTGGTCAAATTGGGGGGAGGTGCTGGGAGTAAAATACTGAATATATG

AGTTTCAGTTGAAAAAAAAAAAAAAA

FIG. 20  
(CONTINUED)

3601 ATCGATTGGGCCGAGATCTCGCGCGAGGGCTGCCATGGGACCCACTGCAGGGCAGC  
TAGCTAACCGGGCTCTAGAGCGCGCTCCGGACGGTACCCCTGGGTGACGTCCCCGTCG  
^  
3615 3636  
BGL2 NCO1

3661 TGGGANGCTGCAGGCCTCAGGTCCCAGTGGGTTGCCATCTGCCAGTAGAAACCTGATGT  
ACCCTNCGACGTCCGAAGTCCAGGGTACCCCCAACGGTAGACGGTCATCTTGACTACA

3721 AGAATCAGGGCGCAGGTGTGGACACTGTCCCTGAATCTCAATGTCTCAGTGTGCTGAAA  
TCTTAGTCCCAGCCTCACACCTGTGACAGGACTTAGAGTTACAGAGTCACACACGACTTT

3781 CATGTAGAAATTAAAGTCCATCCCTCCTACTCTACTGGGATTGAGCCCCCTCCCTATCCC  
GTACATCTTAATTTCAGGTAGGGAGGATGAGATGACCTAACTCGGGAAGGGATAGGG

3841 CCCCCAGGGGCAGAGGAGTCCCTCTCACTCCTGTGGAGGAAGGAATGATACTTGTATT  
GGGGTCCCCGTCTCCTCAAGGAGAGTGAGGACACCTCCTTACTATGAAACAATAA

\*\*\*\*\*

3901 TTCACTGCTGGTACTGAATCCACTGTTCATTTGTTGGTTGTTGTTGAGA  
AAAGTGACGACCATGACTTAGGTGACAAAGTAAACAACAAACAAACAAACAAACTCT

\*\*\*\*\*

3961 AGCGGTTCACTCTGTTGCTCAGGCTGGANGGAGTGCAATGGCGCGATCTGGCTTACT  
TCGCCAAAGTGAGAACACGAGTCCGACCTNCCTCACGTTACCGCGCTAGAACCGAATGA

ALU

\*\*\*\*\*

4021 GCAGCCTCTGCCTCCCAGGTTCAAGTGATTCTCCTGCTTCCGCCTCCATTGGCTGGGA  
CGTCGGAGACGGAGGGTCCAAGTTCACTAAGAGGACGAAGGCGGAGGGTAAACCGACCT

\*\*\*\*\*

4081 TTACAGGCACCCGCCACCATGCCAGCTAATTGTTGTATTAGTANANACNGGGTG  
AATGTCCGTGGCGGTGGTACGGTCAAGTAAACATAAAATCATNTNTGNCCCCAC

A

=====

4141 GGGGTGGGTTCACATGTTGCCAAGCTGGTCTCGAACTCTGAACATGATCCANC  
CCCCACCCCAAGTGTACAACCGGTTGACAGAGCTGAAGACTTGAGTCTACTAGGTNG

LU

=====

4201 TG CCTCTGCCTCCTAAAATTGCTGGGATTACAGGTGTNANCCACCATGCCAACTCAAAA  
ACGGAGACGGAGGATTTAACGACCTAACGTCCACANTNGGTGGTACGGGTTGAGTTTT

4261 TTTACTCTGTTANAAACATCTGGGTCTAACGGTAGGAANCTCACCCACTCAATTGTTGT  
AAATGAGACAAATNTTGAGACCCAGATTCCATCCTNGAGTGGGTGAGTTAAAACA

4321 GGTGTTTTAAGCCAATNANAAAATTTTNTATGTTGTTNNNNNNNNNNNNNNNNNN  
CCACAAAAATTGGTTANTTTAAAAANTACAACAAANNNNNNNNNNNNNNNNNN  
4381 NNN  
NN  
4441 NNN  
NN  
4501 NNN  
NN  
4561 NNN  
NN  
4621 NNN  
NN  
4681 NNN  
NN  
4741 NNN  
NN  
4801 NNN  
NN  
4861 NNN  
NN  
4921 NNN  
NN  
4981 NNCGGTGNNNGAGGG  
NNNGGCCACNNCTCCC  
5041 NGCCANGRAGGGGCCAGGTTCAANTTCCAACCKTTTWGGARGGACNGCCCCCAGGG  
NCGGTNCYCTCCCCGGTCCAAGGTTNAAGGGTGGMAAAWCCTYCTGNCGGGGTCCC  
5101 GGGGATRAACAGANTGGGGKGGTWGGTTNAKGTCGGAACNCCTNGGCCTGGAG  
CCCCTAYTTGTCTNACCCCCMCCAWCCTAACMCCACCTTGNGGAANCSCGGACCTC  
5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGGCAGGGRAGTTG  
TTGCACGTTCTCCTTACTTCCCGACMCAGTTCTCGGGTTACGCAAGGCCYTC  
5221 CAGGGAGGCCACTCCGGGAGGTCCSGCGTCCCCGTCAGGGAGCAATGCGTCCTCGGG  
GTCCCTCCGTGAGGCCCTCCAGGSCGACGGCAGGTTCCCTCGTTACGCAAGGCC  
5281 TTGTCCTCCAWGCCCGTCTACGCGCCTYCCGTCTCCCTTCACGTTCCGGCATTG  
AAGCAGGGGTWCGGCGCAGATGCGCGARGGCAGGAGGGAAAGTGCAAGGCCGTAAGCAC  
5341 GTGCCCGGAGCCCAGCCTGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG  
CACGGGCCTCGGGCTGCCGGCAGGCCTGGACCTCCGTGGACCCAGAGGCCAGTC  
5401 GCCAGCGGCCAAAGGGTCGCCGACGCACCTGTTCCAGGGCCTCCACATCATGGCC  
CGTCGCCGGTTCCAGCGCGTGCCTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

FIG. 21  
(CONTINUED)

5461 CCCTCGGGTTACCCCCACAGCCTAGGCCGATTGACCTCTCTCCGCTGGGGCCCTCGCCT  
GGGAGCCCAATGGGGTGTGGATCCGGCTAACGCTGGAGAGAGGCAGCCCCGGGAGCGGA

Sp1

\*\*\*\*\*

5521 GCGTCCCTGCACCCCTGGGAGCGCGAGCGCGCGCGGGGGAGCGCGGCCATACCC  
CCGCAGGGACGTGGGACCCCTCGCGCTGCCGCCGCCCTTCGGCCGGTATGGG

5581 CGGGTCCGCCCGGAAGCAGCTGCGCTGTCGGGCCAGGCCGGCTCCAGTGGATTGCG  
GGCCCAGGCGGGCTCGTCACGCGACAGCCCCGGTCCGGCCGAGGGTCACCTAACGCG

Topo\_II\_cleavage\_site

\*\*\*\*\*

5641 GGGCACAGACGCCAGGACCAGCGCTTCCCACGTGGCGGAAGGACTGGGACCCGGGACC  
CCCGTGTCTGCGGGTCCTGGCGAAGGGTGACCGCTTCTGACCCCTGGGGCGTGG

E2F

\*\*\*\*\*

5701 CGTCCTGCCCTTCACCTCAGCTCCGCTTCTCCGCGGGACCCGGCCCGTCCGAA  
GCAGGACGGGAAGTGGAAAGGTCGAGGCGAAGAAGGCGCCCTGGGCCGGGAGGGCTT

E

\*\*\*\*

5761 CCCTCCCAGGTCCCGGCCAGCCCTTCCGGCCCTCCAGCCCTCCCTTCTTC  
GGGAAGGGTCCAGGGCCGGTCGGGAAGGCCGGAGGGTCGGGGAGGGGAAGGAAAAG

Sp1

=====

2F

\*\*\*\*\*

NFkB

h

\*\*\*\*\*

5821 CGCGCCCCGCCCTCTCCTCGCGCGAGTTTCAGGCAGCGCTCGTCCTGCTGCGCA  
GCGCGGGCGGGAGAGGAAGCGCCGCTCAAAGTCCGTCGCGACGCAGGACGACGCGT

5860

5875

ECO47III

FSP1

TRTS :

\*\*\*\*\*>

5881 CGTGGGAAGCCCTGGCCCCGGCACCCCGCGATGCCGCGCGCTCCCGCTGCCGAGGCC  
GCACCCCTCGGGACCGGGCCGGTGGGGCGCTACGGCGCCGAGGGCGACGGCTCGGC

5941 TGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGCCACGTTGTGCGGC  
ACCGAGGGACGACCGCTGGTGATGGCGCTCCACGACGGGACCGGTGCAAGCACGCCG

5953  
FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGAGCGCGGGGACCCGGGGCTTCCGCGCG  
CGGACCCGGGTCCGACCGCCGACCATCGCGCCCTGGGCCGAAAGGCGCGCG

6061 TGGTGGCCCAAGTGCCTGGTGTGCGTGCCTGGGACGCACGCCGCCCGCCGCCCCCT  
ACCAACCGGGTACGGACCACACGCACGGGACCGCTCGTGCCTGGGGGGCGGGGGGA

NFkB

=====

FIG. 21  
(CONTINUED)

\*\*\*\*\*  
6121 CCTTCCGCCAGGTGGCCTCCCCGGGTCGGCGTCGGCTGGGTTGAGGCAGGCCGGGG  
GGAAGGCGGTCCACCCGGAGGGGCCAGCCGAGGCCAACCCAACTCCCGCCGGCCCC

Topo\_II\_cleavage\_s

: : : : : : : : :

NFKB

=====

Intron1

\*\*\*\*\*>

6181 GGAACCAGCGACATGGGAGAGCAGCGCAGGCAGCTCAGGGCGCTCCCCCGCAGGTGTC  
CCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCAAGGGGGCGTCCACAG

ite

:

6241 CTGCCTGAAGGAGCTGGTGGCCCAGTGCTGCAGAGGCTGTGCGAGCGCGCGAAGAA  
GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCGACACGCTCGCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGGCTGCTGGACGGGCCCCGGGGGGCCCCCGAGGCCTT  
GCACGACCGGAAGCGAAGCGCAGCACCTGCCCGGGCGCCCCGGGGCTCCGGAA

6361 CACCACCAGCGTGCAGCTACCTGCCAACACCGTGACCGACGCACGTGCGGGGGAGCGG  
GTGGTGGTCGACCGCTGATGGACGGTTGTGCCACTGGCTCGTGACGCCCTCGCC  
^

6372

FSP1

6421 GCGTGGGGCTGCTGCTGCCCGCGTGGCGACGACGTGCTGGTTACCTGCTGGCACG  
CCGCACCCCCGACGACGACGCCCGCTGCTGACGACCAAGTGGACGACCGTGC

6481 CTGCGCGCTTTGTGCTGGCTCCAGCTGCCCTACCAAGGTGTGCGGGCCGCGCT  
GACGCGCAGAAACACGACCAACCGAGGGTCGACCGGGATGGTCCACACGCCGGCGA

6541 GTACCAGCTCGCGCTGCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCCGAAG  
CATGGTCAGCCGCACGGTGAGTCCGGCCGGGCGGTGTGCGATCACCTGGGCTTC

6601 GCGTCTGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGG  
CGCAGACCCCTACGCTGCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCCGGGGCAGTGCCAGCGAAGTCTGCCGTGCC  
GGACGGTCGGGCCACGCTCCGCCGGCCCCGTACGGTCGGCTCAGACGGCAACGG

6721 CAAGAGGCCAGCGTGGCGCTGCCCTGAGCCGGAGCGGACGCCGGTTGGCAGGGTC  
GTCTCCGGGTCCGCACCGCGACGGGACTCGGCCCTGCCCTGGCAACCGTCCCCAG

6781 CTGGGCCACCGGGCAGGACCGCTGGACCGAGTGACCGTGGTTCTGTGTGGTCACC  
GACCCGGGTGGGCCCTGCGCACCTGGCTACTGGCACCAAAGACACACCACAGTGG

6841 TGCCAGACCCGCCAGAACAGCCACCTCTTGGAGGGTGCCTCTGGCACGCCACTC  
ACGGTCTGGCGCTCTCGGTGGAGAACCTCCCACGCGAGAGACCGTGCAGCGGTGAG

6901 CCACCCATCCGTGGCCGCCAGCACCAACGCCGGCCCCCATCCACATCGCGGCCACCACG  
GGTGGTAGGCACCCGGCGTCGTGGTGCAGGCCGGGGTAGGTGTAGCGCCGGTGGTGC

FIG. 21  
(CONTINUED)

6961 TCCCTGGGACACGCCCTGTCCCCGGTGTACGCCGAGACCAAGCACTTCCTACTCCTC  
AGGGACCCCTGTGCGGAACAGGGGGCACATGCGGCTCTGGTCGTGAAGGAGATGAGGAG  
7021 AGGCAGACAAGGAGCAGCTGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGAC  
TCCGCTGTTCTCGTCACGCCGGAGGAAGGATGAGTCGAGAGACTCCGGTCGGACTG  
7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGAC  
ACCGCAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCGGGACCTACGGTCCCTG  
7141 TCCCCGCAGGTTGCCCGCCTGCCAGCGCTACTGGCAAATGCCGCCCTGTTCTGGA  
AGGGCGTCCAACGGGCGGACGGGTCGCGATGACCGTTACGCCGGGACAAAGACCT

7167  
ECO47III

7201 GCTGCTTGGAACCCACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACGCCGCT  
CGACGAACCCCTGGTGCCTGCGTCACGGGATGCCACAGGAGTTCTGCGTGACGGCGA  
7261 GCGAGCTGCCGTACCCCAGCAGCCGGTGTCTGCCCCGGAGAACGCCAGGGCTCTGT  
CGCTCGACGCCAGTGGGTCGTCGGCCACAGACACGGGCCCTTCGGGTCCCCGAGACA  
7321 GGCAGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCTGGTGAGCTGCTCCGCCAGCA  
CCGCCGGGGCTCCTCCTGTGTCTGGGGCAGCGGACACGTCGACGAGGCCGTG  
7381 CAGCAGCCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCCTGCGCCGGCTGGTCCCCC  
GTCGTGGGACCGTCCACATGCCAAGCACGCCGGACGGACGCCGACACGGGG  
7441 AGGCCTCTGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCAT  
TCCGGAGACCCCGAGGTCCGTGTTGCTGCGCGAAGGAGTCCTGTGGTTCTCAAGTA  
7501 CTCCCTGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG  
GAGGGACCCCTCGTACGGTTCGAGAGCGACGTCCACTGCACCTTACTCGCACGC

\*\*\*\*\*  
7561 GGACTGCGTTGGCTGCGCAGGAGCCAGGTGAGGAGGTGGCGCTCGAGGGCCAGG  
CCTGACGCGAACCGACGCGTCCCTGGTCCACTCCTCCACCAACCGCAGCTCCGGTCC

7575  
FSP1

Intron2

\*\*\*\*\*  
7621 CCCAGAGCTGAATGCAGTAGGGCTCAGAAAAGGGGGCAGGCAGGCCCTGGCCTCCT  
GGGTCTCGACTACGTACCGTCCCTGGTCCACTCCTCCACCAACCGCAGCTCCGGTCC

\*\*\*\*\*  
7681 GTCTCCATCGTCACGTGGCACACGTGGCTTTCGCTCAGGACGTCGAGTGGACACGGTG  
CAGAGGTAGCAGTGCACCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGCCAC

\*\*>  
7741 ATCGAGGTCGACTCTAGAGGATCCCCGGTACCGAGCTCGAATTGTAATCATGGTCATA  
TAGCTCCAGCTGAGATCTCCTAGGGGCCATGGCTCGAGCTTAAGCATTAGTACCAAGTAT

7747  
SAL1

FIG. 21  
(CONTINUED)

32/34

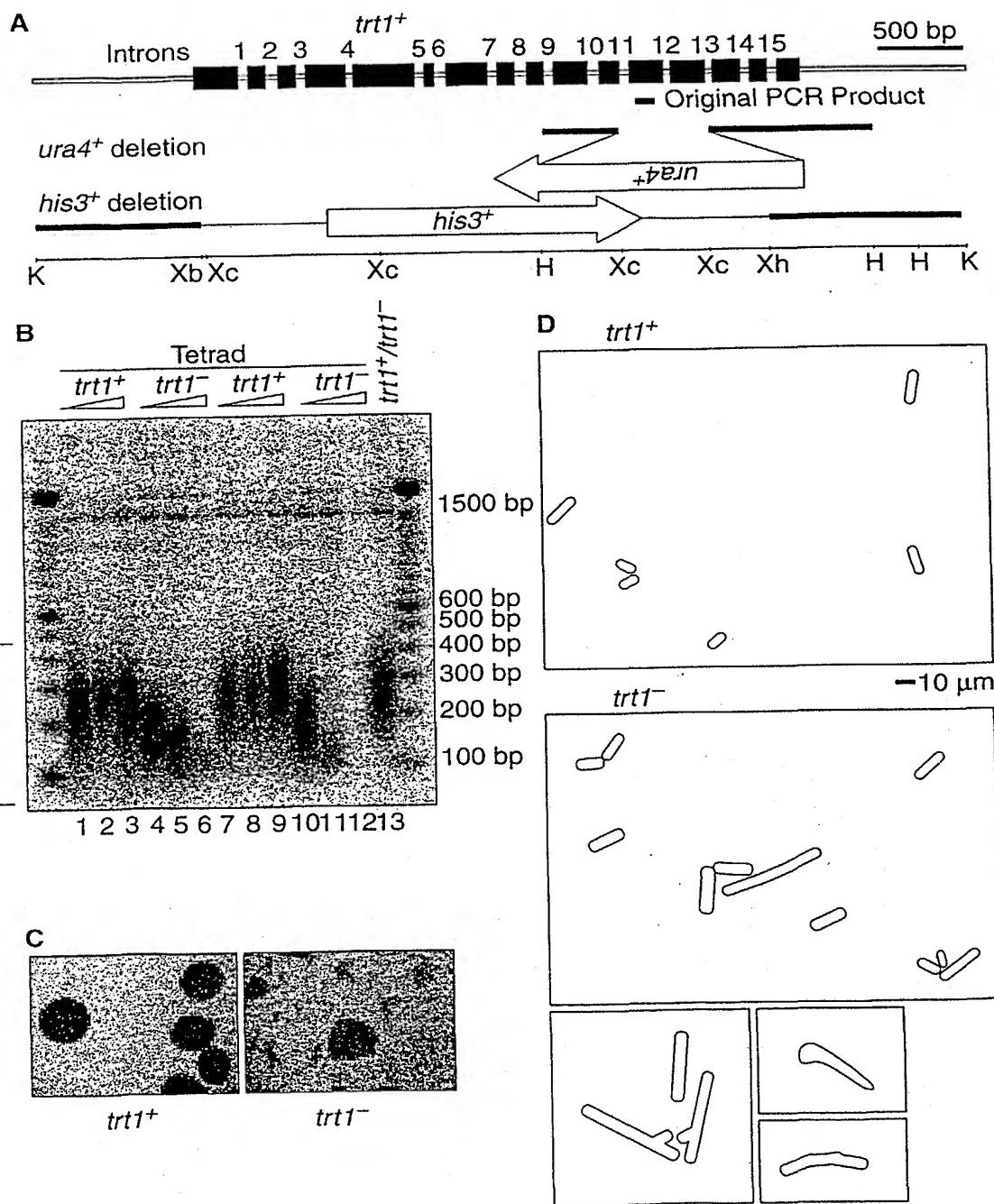


FIG. 22

33/34

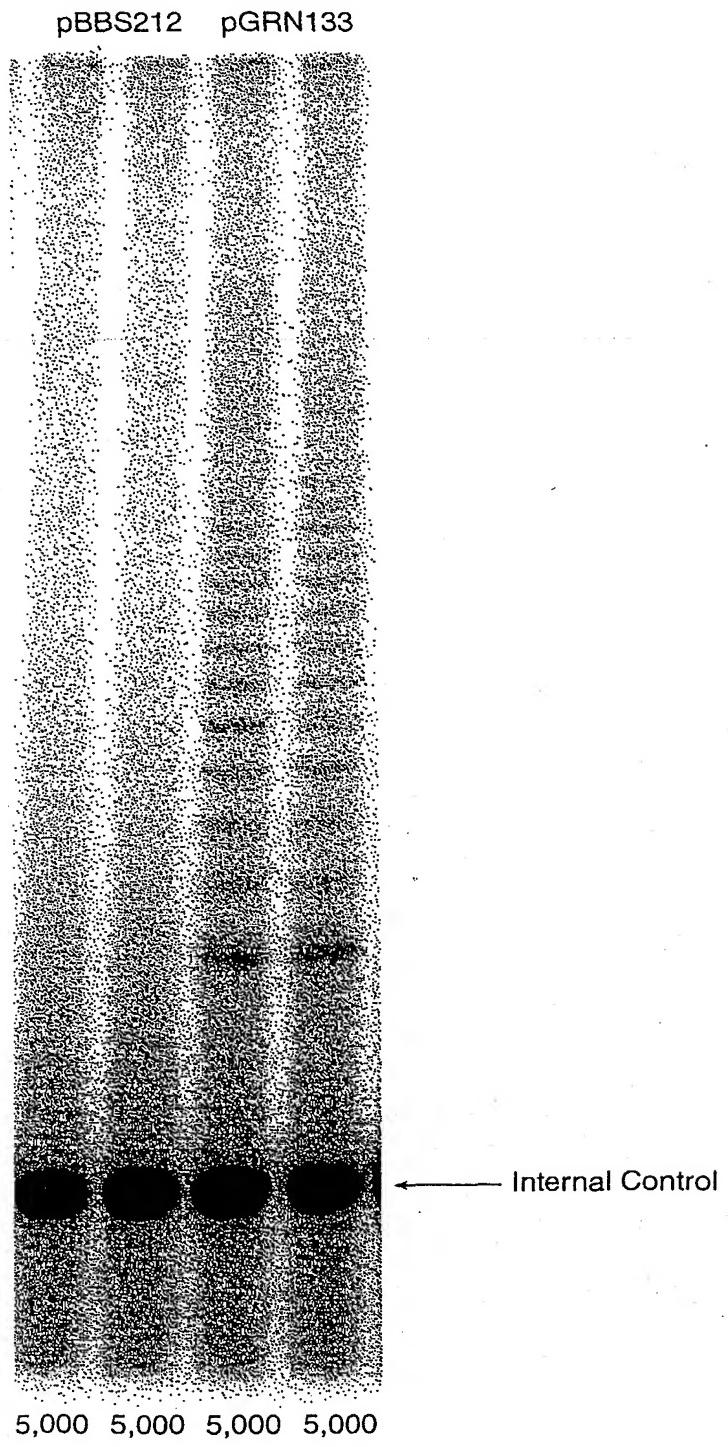
gccaaagttcctgcactggctgatgagtgtacgtcgctcgagctgctcaggcttttttatgtcacggagaccacgttcaaaaagaacacagctcttttctaccggaagagtgctggagcaagttgcaaaagcattgaaatcagacagcacttgaagagggtgcagctgcggacgtgtcggaaagcagaggtcaggcagcatcgggaagccaggccccctgtgacgtccagactcgcttcatccccaaagcctgacgggctgcggccattgtgaacatggactacgtcgtggagccagaacgttcccgagagaaaagagggccgagcgtctcacctcgagggtgaaggcactgttcagcgtctcaactacgagcggcgcg

*FIG. 23*

RECORDED IN FEDERAL FILE

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTCGTGGCTCACCTGCAGGAGACCAGCCCCCTGAGGGATGCCGTCGTACAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCCTTTGACGTCTCCTACGCTTCATGTGCCACCAACGCCGTGCGCATCAGGGGCAAGTC

*FIG. 24*



*FIG. 25*